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The Regents of the University of California

<120> LNP, a Protein Involved in the Initiation of
Mycorrhizal Infection in Plants

<130> 023070-079820US

<140> US 09/657,631
<141> 2000-09-06

<160> 14

<170> PatentIn Ver. 2.1

<210> 1
<211> 1643
<212> DNA
<213> Dolichos biflorus

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<222> (51)...(1439)
<223> lectin nucleotide phosphohydrolase (LNP, NBP46 or
DB46) root lectin

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<222> (195)...(1436)

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Trp Val Trp Pro Lys Thr Lys Ser Met Ser Phe Leu Leu Leu Ile Thr
-45 -40 -35

ttt cta ctc ttc tca ttg cca aaa ctt tct tct tcg caa tat gtt ggg 152
Phe Leu Leu Phe Ser Leu Pro Lys Leu Ser Ser Gln Tyr Val Gly
-30 -25 -20 -15

aac agt atc tta cta aat cat cgt aag ata ctt ccc aac cag gaa ctc 200
Asn Ser Ile Leu Leu Asn His Arg Lys Ile Leu Pro Asn Gln Glu Leu
-10 -5 -1 1

ctt acc tct tac gct atc ttt gat gct ggt agc tct ggg agt cgt 248
Leu Thr Ser Tyr Ala Val Ile Phe Asp Ala Gly Ser Ser Gly Ser Arg
5 10 15

gtc cat gtc ttc aat ttt gac cag aac tta gat ctc ctg cac att ggc 296
Val His Val Phe Asn Phe Asp Gln Asn Leu Asp Leu Leu His Ile Gly
20 25 30

aat gac ctc gag ttt aca aaa aag atc aaa ccc ggt ttg agc tca tac 344
Asn Asp Leu Glu Phe Thr Lys Lys Ile Lys Pro Gly Leu Ser Ser Tyr
35 40 45 50

gct gat aag cct gaa aaa gct gca gaa tct ctc att cca ctt ttg gag Ala Asp Lys Pro Glu Lys Ala Ala Glu Ser Leu Ile Pro Leu Leu Glu 55	60	65	392
gaa gct gaa gat gtt gtc cct gag gaa ctg cac ccc aag aca ccc ctt Glu Ala Glu Asp Val Val Pro Glu Glu Leu His Pro Lys Thr Pro Leu 70	75	80	440
aag ctt ggg gca aca gca ggt ttg agg ctc ttg gat ggg gat gct gct Lys Leu Gly Ala Thr Ala Gly Leu Arg Leu Leu Asp Gly Asp Ala Ala 85	90	95	488
gaa aag ata ttg caa gcg gtt agg gaa atg ttc agg aac aga agt tcc Glu Lys Ile Leu Gln Ala Val Arg Glu Met Phe Arg Asn Arg Ser Ser 100	105	110	536
ctg agc gtt caa cct gat gca gta tct gtt att gat gga acc caa gaa Leu Ser Val Gln Pro Asp Ala Val Ser Val Ile Asp Gly Thr Gln Glu 115	120	125	584
ggt tct tac tta tgg gtt aca gtt aac tat ctg tta gga aag ttg gga Gly Ser Tyr Leu Trp Val Thr Val Asn Tyr Leu Leu Gly Lys Leu Gly 135	140	145	632
aag aag ttt aca aaa act gtg gga gtg ata gat ctt gga ggt gct tca Lys Lys Phe Thr Lys Thr Val Gly Val Ile Asp Leu Gly Gly Ala Ser 150	155	160	680
gtt caa atg gct tat gct gtc tca aga aat aca gct aaa aat gcc cca Val Gln Met Ala Tyr Ala Val Ser Arg Asn Thr Ala Lys Asn Ala Pro 165	170	175	728
aaa cca cca caa gga gag gat cca tac atg aag aag ctt gta ctc aag Lys Pro Pro Gln Gly Glu Asp Pro Tyr Met Lys Lys Leu Val Leu Lys 180	185	190	776
gga aag aaa tat gac ctt tat gtt cac agt tac ttg cgt tat ggt aac Gly Lys Lys Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Tyr Gly Asn 195	200	205	824
gac gca gca cgt gtt aag att ttt aag acc act gat ggt gct gct agt Asp Ala Ala Arg Val Lys Ile Phe Lys Thr Thr Asp Gly Ala Ala Ser 215	220	225	872
cct tgt cta ttg gca ggc tat gaa gat ata tac aga tat tcc gga gaa Pro Cys Leu Leu Ala Gly Tyr Glu Asp Ile Tyr Arg Tyr Ser Gly Glu 230	235	240	920
tgc tac aat atc tat ggt ccc act tct ggt gcc aac ttt aat gag tgc Ser Tyr Asn Ile Tyr Gly Pro Thr Ser Gly Ala Asn Phe Asn Glu Cys 245	250	255	968
cgt gac cta gct ctt cag att ctc aga ttg aat gag cca tgt tcc cat Arg Asp Leu Ala Leu Gln Ile Leu Arg Leu Asn Glu Pro Cys Ser His 260	265	270	1016
gaa aac tgc acc ttt ggt ggg ata tgg gat ggt gga aaa gga agt gga Glu Asn Cys Thr Phe Gly Gly Ile Trp Asp Gly Gly Lys Gly Ser Gly 275	280	285	1064
		290	

cag aaa aac ctt gtt act tca gct ttc tac tat agg tct tct gag	1112		
Gln Lys Asn Leu Val Val Thr Ser Ala Phe Tyr Tyr Arg Ser Ser Glu			
295	300	305	
gtt ggt ttt gtc act cct ccc aat tcc aaa aat cgc cct ctg gat ttt	1160		
Val Gly Phe Val Thr Pro Pro Asn Ser Lys Asn Arg Pro Leu Asp Phe			
310	315	320	
gaa act gca gct aaa caa gct tgt agt tta aca ttc gag gaa gcg aaa	1208		
Glu Thr Ala Ala Lys Gln Ala Cys Ser Leu Thr Phe Glu Glu Ala Lys			
325	330	335	
tcc act ttt cca aat gtt gag aaa gat aaa ctt cca ttt gta tgc gtg	1256		
Ser Thr Phe Pro Asn Val Glu Lys Asp Lys Leu Pro Phe Val Cys Val			
340	345	350	
gat ttc aca tac cag tat aca ttg ctt gtt gat gga ttt ggc cta gat	1304		
Asp Phe Thr Tyr Gln Tyr Thr Leu Leu Val Asp Gly Phe Gly Leu Asp			
355	360	365	370
cca gag caa gag att aca gtg gca gaa gga att gaa tat caa gat gcc	1352		
Pro Glu Gln Glu Ile Thr Val Ala Glu Gly Ile Glu Tyr Gln Asp Ala			
375	380	385	
att gtg gaa aca gca tgg cct cta gga act gcc ata gaa gcc ata tca	1400		
Ile Val Glu Thr Ala Trp Pro Leu Gly Thr Ala Ile Glu Ala Ile Ser			
390	395	400	
tct ttg cct aaa ttt aat cgt cta atg tat ttt atc taa gccatgtcct	1449		
Ser Leu Pro Lys Phe Asn Arg Leu Met Tyr Phe Ile			
405	410	415	
ccacttatga ccacttaat taaaataaaa ctcacccttt tcactaaaaa aaaaaaaaaa	1509		
aaaagtcctt ttttattcca ttgagtatca agtgttaatt tgtttctgac aaatggaggt	1569		
gtaaaaagtga aacaaagtat gttttgtca gatacgaatg gaagtagggt tatgatgaaa	1629		
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<210> 2
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 <213> Dolichos biflorus

<220>
 <223> lectin nucleotide phosphohydrolase (LNP, NBP46 or
 DB46) root lectin

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 Ile Thr Phe Leu Leu Phe Ser Leu Pro Lys Leu Ser Ser Ser Gln Tyr
 20 25 30
 Val Gly Asn Ser Ile Leu Leu Asn His Arg Lys Ile Leu Pro Asn Gln
 35 40 45
 Glu Leu Leu Thr Ser Tyr Ala Val Ile Phe Asp Ala Gly Ser Ser Gly
 50 55 60
 Ser Arg Val His Val Phe Asn Phe Asp Gln Asn Leu Asp Leu Leu His
 65 70 75 80

Ile Gly Asn Asp Leu Glu Phe Thr Lys Lys Ile Lys Pro Gly Leu Ser
 85 90 95
 Ser Tyr Ala Asp Lys Pro Glu Lys Ala Ala Glu Ser Leu Ile Pro Leu
 100 105 110
 Leu Glu Glu Ala Glu Asp Val Val Pro Glu Glu Leu His Pro Lys Thr
 115 120 125
 Pro Leu Lys Leu Gly Ala Thr Ala Gly Leu Arg Leu Leu Asp Gly Asp
 130 135 140
 Ala Ala Glu Lys Ile Leu Gln Ala Val Arg Glu Met Phe Arg Asn Arg
 145 150 155 160
 Ser Ser Leu Ser Val Gln Pro Asp Ala Val Ser Val Ile Asp Gly Thr
 165 170 175
 Gln Glu Gly Ser Tyr Leu Trp Val Thr Val Asn Tyr Leu Leu Gly Lys
 180 185 190
 Leu Gly Lys Lys Phe Thr Lys Thr Val Gly Val Ile Asp Leu Gly Gly
 195 200 205
 Ala Ser Val Gln Met Ala Tyr Ala Val Ser Arg Asn Thr Ala Lys Asn
 210 215 220
 Ala Pro Lys Pro Pro Gln Gly Glu Asp Pro Tyr Met Lys Lys Leu Val
 225 230 235 240
 Leu Lys Gly Lys Lys Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Tyr
 245 250 255
 Gly Asn Asp Ala Ala Arg Val Lys Ile Phe Lys Thr Thr Asp Gly Ala
 260 265 270
 Ala Ser Pro Cys Leu Leu Ala Gly Tyr Glu Asp Ile Tyr Arg Tyr Ser
 275 280 285
 Gly Glu Ser Tyr Asn Ile Tyr Gly Pro Thr Ser Gly Ala Asn Phe Asn
 290 295 300
 Glu Cys Arg Asp Leu Ala Leu Gln Ile Leu Arg Leu Asn Glu Pro Cys
 305 310 315 320
 Ser His Glu Asn Cys Thr Phe Gly Gly Ile Trp Asp Gly Gly Lys Gly
 325 330 335
 Ser Gly Gln Lys Asn Leu Val Val Thr Ser Ala Phe Tyr Tyr Arg Ser
 340 345 350
 Ser Glu Val Gly Phe Val Thr Pro Pro Asn Ser Lys Asn Arg Pro Leu
 355 360 365
 Asp Phe Glu Thr Ala Ala Lys Gln Ala Cys Ser Leu Thr Phe Glu Glu
 370 375 380
 Ala Lys Ser Thr Phe Pro Asn Val Glu Lys Asp Lys Leu Pro Phe Val
 385 390 395 400
 Cys Val Asp Phe Thr Tyr Gln Tyr Thr Leu Leu Val Asp Gly Phe Gly
 405 410 415
 Leu Asp Pro Glu Gln Glu Ile Thr Val Ala Glu Gly Ile Glu Tyr Gln
 420 425 430
 Asp Ala Ile Val Glu Thr Ala Trp Pro Leu Gly Thr Ala Ile Glu Ala
 435 440 445
 Ile Ser Ser Leu Pro Lys Phe Asn Arg Leu Met Tyr Phe Ile
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<210> 3
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 <212> DNA
 <213> *Medicago sativa*

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 <222> (1)..(1458)
 <223> full length clone

<220>
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 <222> (13)..(1380)
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 root lectin

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ctc ttg tta atg cct gca atc act tcc tcc caa tat tta gga aac aac 96
 Leu Leu Leu Met Pro Ala Ile Thr Ser Ser Gln Tyr Leu Gly Asn Asn
 20 25 30

cta ctc act aat cga aag att ttc caa aaa caa gaa acc tta acc tct 144
 Leu Leu Thr Asn Arg Lys Ile Phe Gln Lys Gln Glu Thr Leu Thr Ser
 35 40 45

tac gct gtc ata ttt gat gct ggt agc act ggt act cgt gtc cat gtt 192
 Tyr Ala Val Ile Phe Asp Ala Gly Ser Thr Gly Thr Arg Val His Val
 50 55 60

tac cat ttt gat cag aac tta gat cta ctt cac att ggc aat gat att 240
 Tyr His Phe Asp Gln Asn Leu Asp Leu Leu His Ile Gly Asn Asp Ile
 65 70 75 80

gag ttt gtt gac aag atc aaa cca ggt ttg agt gca tat ggg gat aat 288
 Glu Phe Val Asp Lys Ile Lys Pro Gly Leu Ser Ala Tyr Gly Asp Asn
 85 90 95

cct gaa caa gca gca aaa tct ctc att cca ctt ttg gag gaa gca gaa 336
 Pro Glu Gln Ala Ala Lys Ser Leu Ile Pro Leu Leu Glu Ala Glu
 100 105 110

gat gtg gtt cct gag gat ctg cac ccc aaa aca ccc ctt agg ctt ggg 384
 Asp Val Val Pro Glu Asp Leu His Pro Lys Thr Pro Leu Arg Leu Gly
 115 120 125

gca acc gca ggt ttg agg ctt ttg aat ggg gat gct gct gaa aag ata 432
 Ala Thr Ala Gly Leu Arg Leu Leu Asn Gly Asp Ala Ala Glu Lys Ile
 130 135 140

ttg caa gcg aca agg aat atg ttc agc aac aga agt acc ctc aac gtt 480
 Leu Gln Ala Thr Arg Asn Met Phe Ser Asn Arg Ser Thr Leu Asn Val
 145 150 155 160

caa cgt gat gca gtt tct att att gat gga acc caa gaa ggt tct tat 528
 Gln Arg Asp Ala Val Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr
 165 170 175

atg tgg gtg aca gtt aac tat gta ttg ggg aat ttg gga aaa agc ttc 576
 Met Trp Val Thr Val Asn Tyr Val Leu Gly Asn Leu Gly Lys Ser Phe
 180 185 190

aca aaa tca gtg gga gta att gac ctt gga ggt ggt tca gtt caa atg 624
 Thr Lys Ser Val Gly Val Ile Asp Leu Gly Gly Ser Val Gln Met
 195 200 205

aca tat gca gtg tca aag aaa aca gca aaa aat gct cct aaa gtt gct	672
Thr Tyr Ala Val Ser Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala	
210 215 220	
gat gga gag gat cca tat att aag aag ctt gtg ctc aag gga aag caa	720
Asp Gly Glu Asp Pro Tyr Ile Lys Lys Leu Val Leu Lys Gly Lys Gln	
225 230 235 240	
tat gat ctc tat gtt cat agt tac ttg cgt ttt ggc aaa gaa gca act	768
Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Phe Gly Lys Glu Ala Thr	
245 250 255	
cga gca cag gtt ttg aat gca act aat gga tct gct aac cct tgc att	816
Arg Ala Gln Val Leu Asn Ala Thr Asn Gly Ser Ala Asn Pro Cys Ile	
260 265 270	
tta cct gga ttt aat ggg acc ttt aca tat tca gga gtg gag tat aag	864
Leu Pro Gly Phe Asn Gly Thr Phe Thr Tyr Ser Gly Val Glu Tyr Lys	
275 280 285	
gct ttt tcc cct tct tct ggc tcc aac ttt gat gat tgc aaa gaa ata	912
Ala Phe Ser Pro Ser Ser Gly Ser Asn Phe Asp Asp Cys Lys Glu Ile	
290 295 300	
att ctt aag gtt ctt aaa gta aat gat cca tgt ccc tat ccg agt tgc	960
Ile Leu Lys Val Leu Lys Val Asn Asp Pro Cys Pro Tyr Pro Ser Cys	
305 310 315 320	
act ttt ggt gga ata tgg aat ggt gga gga ggg agt gga caa aaa aaa	1008
Thr Phe Gly Gly Ile Trp Asn Gly Gly Ser Gly Gln Lys Lys	
325 330 335	
ctt ttt gtt act tca gct ttc gct tac ctg gct gaa gat gtt ggt atg	1056
Leu Phe Val Thr Ser Ala Phe Ala Tyr Leu Ala Glu Asp Val Gly Met	
340 345 350	
gtt gag cca aat aaa cct aat tcc ata ctt cat cca gta gat ttc gaa	1104
Val Glu Pro Asn Lys Pro Asn Ser Ile Leu His Pro Val Asp Phe Glu	
355 360 365	
att gaa gct aag cga gct tgt gca tta aac ttt gag gat gtc aaa tcc	1152
Ile Glu Ala Lys Arg Ala Cys Ala Leu Asn Phe Glu Asp Val Lys Ser	
370 375 380	
act tat cct cga ctt acg gat gca aaa cgt cca tat gta tgc atg gat	1200
Thr Tyr Pro Arg Leu Thr Asp Ala Lys Arg Pro Tyr Val Cys Met Asp	
385 390 395 400	
ctc tta tac caa cat gtg ttg ctt gtt cat gga ttt ggc tta ggt cca	1248
Leu Leu Tyr Gln His Val Leu Leu Val His Gly Phe Gly Leu Gly Pro	
405 410 415	
cga aaa gag att aca gta ggt gag gga att caa tat cag aat tct gtt	1296
Arg Lys Glu Ile Thr Val Gly Glu Gly Ile Gln Tyr Gln Asn Ser Val	
420 425 430	
gtg gaa gct gca tgg cct cta ggt act gcc gtg gaa gcc ata tca gcg	1344
Val Glu Ala Ala Trp Pro Leu Gly Thr Ala Val Glu Ala Ile Ser Ala	
435 440 445	

tta cct aag ttt aag cga tta atg tat ttt att taa gct ttt aga gat 1392
Leu Pro Lys Phe Lys Arg Leu Met Tyr Phe Ile Ala Phe Arg Asp
450 455 460

gtc aag ata ttt cag taa cag cta act tta tca aaa att aaa taa aac 1440
Val Lys Ile Phe Gln Gln Leu Thr Leu Ser Lys Ile Lys Asn
465 470 475 480

tgg cgc att ttg tct ttc 1458
Trp Arg Ile Leu Ser Phe
485

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<211> 459
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<213> *Medicago sativa*

<220>
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root lectin

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20 25 30
Leu Leu Thr Asn Arg Lys Ile Phe Gln Lys Gln Glu Thr Leu Thr Ser
35 40 45
Tyr Ala Val Ile Phe Asp Ala Gly Ser Thr Gly Thr Arg Val His Val
50 55 60
Tyr His Phe Asp Gln Asn Leu Asp Leu Leu His Ile Gly Asn Asp Ile
65 70 75 80
Glu Phe Val Asp Lys Ile Lys Pro Gly Leu Ser Ala Tyr Gly Asp Asn
85 90 95
Pro Glu Gln Ala Ala Lys Ser Leu Ile Pro Leu Leu Glu Ala Glu
100 105 110
Asp Val Val Pro Glu Asp Leu His Pro Lys Thr Pro Leu Arg Leu Gly
115 120 125
Ala Thr Ala Gly Leu Arg Leu Leu Asn Gly Asp Ala Ala Glu Lys Ile
130 135 140
Leu Gln Ala Thr Arg Asn Met Phe Ser Asn Arg Ser Thr Leu Asn Val
145 150 155 160
Gln Arg Asp Ala Val Ser Ile Ile Asp Gly Thr Gln Glu Gly Ser Tyr
165 170 175
Met Trp Val Thr Val Asn Tyr Val Leu Gly Asn Leu Gly Lys Ser Phe
180 185 190
Thr Lys Ser Val Gly Val Ile Asp Leu Gly Gly Ser Val Gln Met
195 200 205
Thr Tyr Ala Val Ser Lys Lys Thr Ala Lys Asn Ala Pro Lys Val Ala
210 215 220
Asp Gly Glu Asp Pro Tyr Ile Lys Lys Leu Val Leu Lys Gly Lys Gln
225 230 235 240
Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Phe Gly Lys Glu Ala Thr
245 250 255
Arg Ala Gln Val Leu Asn Ala Thr Asn Gly Ser Ala Asn Pro Cys Ile
260 265 270
Leu Pro Gly Phe Asn Gly Thr Phe Thr Tyr Ser Gly Val Glu Tyr Lys
275 280 285
Ala Phe Ser Pro Ser Ser Gly Ser Asn Phe Asp Asp Cys Lys Glu Ile
290 295 300

Ile Leu Lys Val Leu Lys Val Asn Asp Pro Cys Pro Tyr Pro Ser Cys
305 310 315 320
Thr Phe Gly Gly Ile Trp Asn Gly Gly Gly Ser Gly Gln Lys Lys
325 330 335
Leu Phe Val Thr Ser Ala Phe Ala Tyr Leu Ala Glu Asp Val Gly Met
340 345 350
Val Glu Pro Asn Lys Pro Asn Ser Ile Leu His Pro Val Asp Phe Glu
355 360 365
Ile Glu Ala Lys Arg Ala Cys Ala Leu Asn Phe Glu Asp Val Lys Ser
370 375 380
Thr Tyr Pro Arg Leu Thr Asp Ala Lys Arg Pro Tyr Val Cys Met Asp
385 390 395 400
Leu Leu Tyr Gln His Val Leu Leu Val His Gly Phe Gly Leu Gly Pro
405 410 415
Arg Lys Glu Ile Thr Val Gly Glu Gly Ile Gln Tyr Gln Asn Ser Val
420 425 430
Val Glu Ala Ala Trp Pro Leu Gly Thr Ala Val Glu Ala Ile Ser Ala
435 440 445
Leu Pro Lys Phe Lys Arg Leu Met Tyr Phe Ile
450 455

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<212> PRT
<213> *Medicago sativa*

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Ala Phe Arg Asp Val Lys Ile Phe Gln
1 5

<210> 6
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<213> *Medicago sativa*

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Gln Leu Thr Leu Ser Lys Ile Lys
1 5

<210> 7
<211> 7
<212> PRT
<213> *Medicago sativa*

<400> 7
Asn Trp Arg Ile Leu Ser Phe
1 5

<210> 8
<211> 1489
<212> DNA
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<222> (1)...(1488)
<223> full length clone

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 <223> lectin nucleotide phosphohydrolase (LNP or NBP46)
 root lectin

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 1 5 10 15

ttc tta att agt ctc atg acc ttt gtg ttc atg tta atg cct gct atc 96
 Phe Leu Ile Ser Leu Met Thr Phe Val Phe Met Leu Met Pro Ala Ile
 20 25 30

tct tcc tcc caa tat ctc gga aac aac att ctc atg aat cgt aag ata 144
 Ser Ser Gln Tyr Leu Gly Asn Asn Ile Leu Met Asn Arg Lys Ile
 35 40 45

tta ctc ccc aaa aat cag gaa cca gtt aca tca tac gct gtt ata ttt 192
 Leu Leu Pro Lys Asn Gln Glu Pro Val Thr Ser Tyr Ala Val Ile Phe
 50 55 60

gat gct ggt agc act gga agc aga gtc cat gtc tac aat ttt gat cag 240
 Asp Ala Gly Ser Thr Gly Ser Arg Val His Val Tyr Asn Phe Asp Gln
 65 70 75 80

aac tta gat ctc ctt ccc gtt gaa aac gaa ctt gag ttt tat gat tcg 288
 Asn Leu Asp Leu Leu Pro Val Glu Asn Glu Leu Glu Phe Tyr Asp Ser
 85 90 95

gtt aaa ccc ggt ttg agt tca tac gct gct aat cct gaa gaa gct gca 336
 Val Lys Pro Gly Leu Ser Ser Tyr Ala Ala Asn Pro Glu Glu Ala Ala
 100 105 110

gaa tct ctg att cca ctt cta aaa gaa gca gaa aat gtg gtt cct gtg 384
 Glu Ser Leu Ile Pro Leu Leu Lys Glu Ala Glu Asn Val Val Pro Val
 115 120 125

agc cag caa ccc aac aca ccc gtt aag ctt ggg gca act gca ggt tta 432
 Ser Gln Gln Pro Asn Thr Pro Val Lys Leu Gly Ala Thr Ala Gly Leu
 130 135 140

agg ctt ttg gag ggg aat gct gct gaa aat ata ttg caa gca gtc agg 480
 Arg Leu Leu Glu Gly Asn Ala Ala Glu Asn Ile Leu Gln Ala Val Arg
 145 150 155 160

gat atg ctc agc aac aga agt gcc ctt aat gtt caa tca gat gca gta 528
 Asp Met Leu Ser Asn Arg Ser Ala Leu Asn Val Gln Ser Asp Ala Val
 165 170 175

tct att ctt gat gga acc caa gaa ggt tct tat ctt tgg gtg aca att 576
 Ser Ile Leu Asp Gly Thr Gln Glu Gly Ser Tyr Leu Trp Val Thr Ile
 180 185 190

aac tat ctc ttg ggg aag ttg gga aaa aga ttt aca aag aca gtg gga 624
 Asn Tyr Leu Leu Gly Lys Leu Gly Lys Arg Phe Thr Lys Thr Val Gly
 195 200 205

gta gtt gat cta gga ggt ggg tca gtg caa atg aca tat gca gtc tca	672
Val Val Asp Leu Gly Gly Ser Val Gln Met Thr Tyr Ala Val Ser	
210 215 220	
agg aac aca gct aaa aat gct cca aaa gta cct gaa gga gag gat cca	720
Arg Asn Thr Ala Lys Asn Ala Pro Lys Val Pro Glu Gly Glu Asp Pro	
225 230 235 240	
tac ata aag aag ctt gta ctc cag gga aag aaa tat gac ctt tat gtt	768
Tyr Ile Lys Lys Leu Val Leu Gln Gly Lys Lys Tyr Asp Leu Tyr Val	
245 250 255	
cac agt tac ttg cgc tat gga aga gaa gca ttt cgt gca gag att ttc	816
His Ser Tyr Leu Arg Tyr Gly Arg Glu Ala Phe Arg Ala Glu Ile Phe	
260 265 270	
aag gtc gct ggt ggt tct gct aat cct tgc att tta gct ggc ttt gat	864
Lys Val Ala Gly Gly Ser Ala Asn Pro Cys Ile Leu Ala Gly Phe Asp	
275 280 285	
ggg gca tat aca tat tcc gga gca gag tat aag gtc tcg gcc cca gct	912
Gly Ala Tyr Thr Tyr Ser Gly Ala Glu Tyr Lys Val Ser Ala Pro Ala	
290 295 300	
tca gga tct aac ttg aat caa tgc aga aag ata gct ctt aag gct ctt	960
Ser Gly Ser Asn Leu Asn Gln Cys Arg Lys Ile Ala Leu Lys Ala Leu	
305 310 315 320	
aaa gtg aat gca cct tgt ccc tat cag aat tgc act ttt ggt ggg ata	1008
Lys Val Asn Ala Pro Cys Pro Tyr Gln Asn Cys Thr Phe Gly Gly Ile	
325 330 335	
tgg aat ggt gga ggt gga agt ggt caa aaa aat ctt ttc ctt act tca	1056
Trp Asn Gly Gly Ser Gly Gln Lys Asn Leu Phe Leu Thr Ser	
340 345 350	
tct ttc tat tac ctc tct gaa gat gtt ggg atc ttt gtg aat aaa ccc	1104
Ser Phe Tyr Tyr Leu Ser Glu Asp Val Gly Ile Phe Val Asn Lys Pro	
355 360 365	
aat gcc aaa att cgt cca gtt gat ttg aag act gca gct aaa cta gct	1152
Asn Ala Lys Ile Arg Pro Val Asp Leu Lys Thr Ala Ala Lys Leu Ala	
370 375 380	
tgt aaa aca aat ctt gag gat gca aaa tcc aaa tac cca gat ctt tat	1200
Cys Lys Thr Asn Leu Glu Asp Ala Lys Ser Lys Tyr Pro Asp Leu Tyr	
385 390 395 400	
gag aaa gac agt gtt gaa tat gtg tgc ttg gat ctt gtc tac gtg tac	1248
Glu Lys Asp Ser Val Glu Tyr Val Cys Leu Asp Leu Val Tyr Val Tyr	
405 410 415	
aca ttg ctt gtt gat gga ttt ggt ctt gat cca ttt caa gag gtt aca	1296
Thr Leu Leu Val Asp Gly Phe Gly Leu Asp Pro Phe Gln Glu Val Thr	
420 425 430	
gtg gcg aat gaa att gaa tat cag gat gct ctt gtg gaa gcc gca tgg	1344
Val Ala Asn Glu Ile Glu Tyr Gln Asp Ala Leu Val Glu Ala Ala Trp	
435 440 445	

cct cta ggc act gcc ata gaa gca ata tca tca ttg cct aaa ttt gag 1392
Pro Leu Gly Thr Ala Ile Glu Ala Ile Ser Ser Leu Pro Lys Phe Glu
450 455 460

aga tta atg tat ttt att taa act act agt acc tgc tta agc ctg gat 1440
Arg Leu Met Tyr Phe Ile Thr Thr Ser Thr Cys Leu Ser Leu Asp
465 470 475 480

tac ctg aag aaa taa aat gaa ata aaa gcc gca tct ttc ttc ctt gct t 1489
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root lectin

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Asn Ile Leu Met Asn Arg Lys Ile Leu Leu Pro Lys Asn Gln Glu Pro
35 40 45
Val Thr Ser Tyr Ala Val Ile Phe Asp Ala Gly Ser Thr Gly Ser Arg
50 55 60
Val His Val Tyr Asn Phe Asp Gln Asn Leu Asp Leu Leu Pro Val Glu
65 70 75 80
Asn Glu Leu Glu Phe Tyr Asp Ser Val Lys Pro Gly Leu Ser Ser Tyr
85 90 95
Ala Ala Asn Pro Glu Glu Ala Ala Glu Ser Leu Ile Pro Leu Leu Lys
100 105 110
Glu Ala Glu Asn Val Val Pro Val Ser Gln Gln Pro Asn Thr Pro Val
115 120 125
Lys Leu Gly Ala Thr Ala Gly Leu Arg Leu Leu Glu Gly Asn Ala Ala
130 135 140
Glu Asn Ile Leu Gln Ala Val Arg Asp Met Leu Ser Asn Arg Ser Ala
145 150 155 160
Leu Asn Val Gln Ser Asp Ala Val Ser Ile Leu Asp Gly Thr Gln Glu
165 170 175
Gly Ser Tyr Leu Trp Val Thr Ile Asn Tyr Leu Leu Gly Lys Leu Gly
180 185 190
Lys Arg Phe Thr Lys Thr Val Gly Val Val Asp Leu Gly Gly Ser
195 200 205
Val Gln Met Thr Tyr Ala Val Ser Arg Asn Thr Ala Lys Asn Ala Pro
210 215 220

Lys Val Pro Glu Gly Glu Asp Pro Tyr Ile Lys Lys Leu Val Leu Gln
 225 230 235 240
 Gly Lys Lys Tyr Asp Leu Tyr Val His Ser Tyr Leu Arg Tyr Gly Arg
 245 250 255
 Glu Ala Phe Arg Ala Glu Ile Phe Lys Val Ala Gly Gly Ser Ala Asn
 260 265 270
 Pro Cys Ile Leu Ala Gly Phe Asp Gly Ala Tyr Thr Tyr Ser Gly Ala
 275 280 285
 Glu Tyr Lys Val Ser Ala Pro Ala Ser Gly Ser Asn Leu Asn Gln Cys
 290 295 300
 Arg Lys Ile Ala Leu Lys Ala Leu Lys Val Asn Ala Pro Cys Pro Tyr
 305 310 315 320
 Gln Asn Cys Thr Phe Gly Gly Ile Trp Asn Gly Gly Gly Ser Gly
 325 330 335
 Gln Lys Asn Leu Phe Leu Thr Ser Ser Phe Tyr Tyr Leu Ser Glu Asp
 340 345 350
 Val Gly Ile Phe Val Asn Lys Pro Asn Ala Lys Ile Arg Pro Val Asp
 355 360 365
 Leu Lys Thr Ala Ala Lys Leu Ala Cys Lys Thr Asn Leu Glu Asp Ala
 370 375 380
 Lys Ser Lys Tyr Pro Asp Leu Tyr Glu Lys Asp Ser Val Glu Tyr Val
 385 390 395 400
 Cys Leu Asp Leu Val Tyr Val Tyr Thr Leu Leu Val Asp Gly Phe Gly
 405 410 415
 Leu Asp Pro Phe Gln Glu Val Thr Val Ala Asn Glu Ile Glu Tyr Gln
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 Asp Ala Leu Val Glu Ala Ala Trp Pro Leu Gly Thr Ala Ile Glu Ala
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 PCR primer

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20

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PCR primer

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17